

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 5, line 5 with the following rewritten paragraph:

Figure FIG. 2 shows the cDNA and deduced amino acid sequences of human *Pin1* and homologies with other WW domain proteins and PPIases. Figure FIG. 2A shows the Pin1 nucleotide sequence (SEQ ID NO: 1) and predicted Pin1 amino acid sequence (SEQ ID NO: 2) (Pin1 indicated in one-letter code). The fusion points between GAL4 and Pin1 in six different isolated clones were: clone H20 at C-9; clone H16.24 and 38 at G+13G+13; clones H6 and H36 at C+15C+15. Underlined residues form a consensus bipartite nuclear localization signal. The N- and C-terminal boxes indicate the WW domain and PPIase domain, respectively. Nucleotide numbers are on the left and amino acid numbers on right. Figure FIG. 2B and 2C shows the alignment of the WW domain (B) and PPIase Domain (C) in selected proteins (from top to bottom SEQ ID NOs: 8-14). FIG. 2C shows the alignment of the PPIase domain in selected proteins (from top to bottom SEQ ID NOs: 15-21). In FIGs. 2B and 2C, identical residues are shown in the bottom row labeled "Consensus" (SEQ ID NO: 22). Dashes indicate gaps introduced to make the alignment. Cbf2, cell binding factor 2; SC, *S. cerevisiae*; EC, *E. coli*; BS, *B. subtilis*; CJ, *C. jejuni*; AT, *A. thaliana*.